CHALLENGES IN UNDERSTANDING CELL COMMUNITIES

DISCUSSIONS AND HOW OUR PROJECT CONTRIBUTES TO THIS APPLICATION

Microorganisms are the most abundant life form on Earth, and they have a significant importance to humans form their role in climate regulation to those of medical importance within the gut [1]. Microorganisms can form intricate communities that can interact and communicate. The communities are naturally very complex with hundreds of species being found in an area. The staggering vastness of the amount of organisms is apparent in the work by Craig Venter where in a sample of water find millions of species. In his Global Ocean Sampling Expedition thus far 60 million genes have been sequenced of bacteria and viruses.

In light of the huge unknown yet to explore focus is aimed at trying to grow to analyse these undefined species. One issue is that some bacteria to be cultivated have specific relationships that are relied on to survive so the ability to grow bacteria together would be beneficial. However this brings an issue in our projects contribution as it requires genetic engineering of bacteria to allow the expression of the surface zinc fingers. In the case of using undescribed species there will not be the possibility of achieving this modification as the genetic sequence can limiting, and the inability to modify genetically.

As mentioned cultivating microbes is an arduous task , yet another hurdle is those microbes that can be grown may have their normal interaction altered by the growth within a laboratory setting. The relationship between bacteria seen in nature can fall into several types such as; commensalism, competition or cooperation [2]. These different strategies also arise within more complex organisms, and so a big question in biology is trying to consider why or in which scenarios it is beneficial to take on a different strategy. Within a laboratory setting a researcher may unintentionally shift the normal interaction. This is apparent in the difference in the survival outcome of a microbial community grown in a mixed community versus a community where bacteria can be spatially organised in microscale environments. In a well-mixed environment the bacteria show more cheating. Another issue that arises is that competition for resources leads to one bacteria outcompeting the others and getting a 'winner-takes-all' situation [3]. I In one example researchers took 2 bacteria to an unstructured community and one with spatial structure achieved by making a tube-like structure with one type of bacteria on the inside and the other bacteria on the outside. Only when the bacteria were structured together were they able to degrade the compounds in their environment [4].

Another example of how the spatial structure of cells influences the use of resources and the growth is in studies that demonstrate that the shape of the colony of yeast can impact the rate of sensing nutrients in the environment and utilising these [5].

A current solution to organising, and confining populations is through technologies such printing bacteria in patches, or via physical separation but allowing them to share an environment[6]. Our project concept is centered on spatial organisation and therefore has relevant potential applications in this area. Our technique if implemented would allow designed control over spatial organisation to a nanoscale level. Most current methods are limited to a micrometer scale, and concerned with discrete patches. Our method would let complex spatial communities be produced with influence over cells and their neighbours. The main challenge to achieve this would be to find the optimal size of DNA bound to a surface to let a single cell bind to one location, with a neighbour of potentially another species nearby. Another concept to tackle, yet is key to synthetic biology, is to have the zinc finger and DNA binding system that can be universally used within a range of microorganisms. The genetic arts we have created and submitted can be utlisied by other iGEM teams and researchers who would be interested in expression this system in other types of bacteria. This would then need to be optimisied so that the cells would all stick with a similar affinity to their assigned location.

References

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